

[illegible]

<213> C. elegans

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29

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<211> 27  
<212> DNA  
<213> C. elegans

<400> 6  
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27

<210> 7  
<211> 876  
<212> DNA  
<213> C. elegans

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ccgcagtatt ggacgatttt attccagaaa tattgggtatc attcgatcac aatatcagtt 180  
ctttattttca ttttaattaa ggtgattcaa aagtttatgg agaatcgaaa accattcact 240  
ttgaaatacc cattgattct ttggaatgga gctcttgacg cattcagtat aattgccaca 300  
ttgcggttct ctattgatcc tctacgatca ctatatgctg aaggattcta caaaactctg 360  
tgctattcgt gtaatccaac tgatgtggct gcattttgga gctttgcatt cgctctttcc 420  
aagattgttg aacttggaga cactatgttc attattttga gaaaacggcc attgatcttt 480  
ttacactact atcatcatgc agcagtgtta atctacactg tccattctgg tgccgagcat 540  
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tactacacag tttctgccat gggatacaga ttaccgaaat gggatcaat gactgtcaca 660  
actgttcaaa caactcaaat gttagctgga gtcggaataa cttggatggg gtacaaagtg 720  
aaaactgaat acaagcttcc ttgtcaacaa tccgtagcca atttgtatct cgcattcgtc 780  
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tcgtcgaaga agtcgaaatc ggtgaagaac gaataa 876

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<211> 1308  
<212> DNA  
<213> C. elegans

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tcaattacag catctgtcgt gtatgtagcc gtcattttta caggaaagaa ggtgggttctc 180  
atctacaaaa aatcacgagt tattactttt gagtctagcc ttcagaatgc aattaagaat 240  
cgaaaccgaa aatcacttaa tagttctcaa atgtttcaga ttatggaaaa gtacaagccc 300  
ttccaactgg acacaccact ctctgtctgg aattcatttt tagccatttt ctcaattctc 360  
gggttctctc gaatgacacc tgaatttcta tggagttggg cagcagaagg aaactcatte 420  
aaatattcaa tttgtcattc atcttatgct caaggagtca ctggtttctg gactgaacaa 480  
ttcgcaatga gcaaactttt cgagctcatc gacacaatct tcatcgttct tcgtaaactg 540  
ccactcatct tcttctactg gtatcatcat gtaactgtta tgatctacac atggcacgcg 600  
tacaaggatc aactgcatc aggacggtgg ttcatgttga tgaattatgg agttcatgct 660  
cttatgtatt cctactatgc tcttctgtct ctgaaattcc gtcttccaaa acaaatggca 720

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gttaagaaaa	acaaccgtac	agtaaattat	gaaaataatt	caaaaaattt	ccccgatctc	960
gttttaattt	acctgagaaa	aaaggtttca	agaaaatcga	aaaatcggca	atgttcagaa	1020
aataattata	aaattcaatt	ttcatcaaat	tttggttaatg	ttgatggaaa	aaaacataag	1080
aaaacatatg	aactttattct	tccaagaaga	aaaatgacca	caattttaac	ttttctatct	1140
ggaaaaaatc	gaattttttc	gaaatatcag	aaaaatcgaa	aaaacatttc	gattcctggt	1200
gatttcgaaa	ttctggagcc	aaaagaagat	atcaatgcta	acatcgctga	gccatccatc	1260
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<210> 9  
 <211> 825  
 <212> DNA  
 <213> C. elegans

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gatctccaaa	atacacttgc	tctctggaac	ttcgggtttt	caactgtctc	gggaatcgcc	240
gcctataagc	ttattccaga	actattcgga	gttttcatga	aggacgggtt	tgtcgtctcc	300
tactgtcaaa	acgagaacta	ctacaccgat	gcatacaactg	gattctgggg	ctgggccttt	360
gtgatgtcga	aagctccaga	actaggggat	actatgttct	tggtccttcg	taaaaaacca	420
gttatcttca	tgcactggta	tcacatgcc	ctcacatttg	tctacgcagt	agtcacatac	480
tctgagcatc	aggcatgggc	tcgttgggtc	ttggctctca	accttgccgt	ccacactgtt	540
atgtatttct	acttcgcctg	tcgcgccttg	aacatccaaa	ctccacgcc	agtggcaaag	600
ttcatcacta	ctattcaaatt	tgccaattt	gtcatctcat	gctacatttt	tgggcatttg	660
gtattcatta	agtctgtcga	ttctgttctc	gggtgcgctg	ttagctggaa	tgtgctatcg	720
atcggaggac	tcattgtacat	cagtattttg	ttcctttttg	ccaagttctt	ctacaaggcc	780
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 <211> 861  
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cttgccgtcg	gatatattgc	cactattttt	ggactgaaat	attatatgaa	agaccgaaaa	180
gccttcgatc	tcagtactcc	attaaacatt	tggaatggta	ttctttcgac	attcagctta	240
ttgggattct	tattcacttt	tcctactttg	ttatcagtta	tcagaaagga	tggatttagt	300
cacacctatt	cccatgtctc	tgagctttac	actgacagta	cctctggata	ttggatcttc	360
ctttgggtta	tctcaaagat	tccggaactt	ttggatacag	tattcattgt	tcttcgcaag	420
agaccactta	ttttcatgca	ctggtaccat	cacgcattga	ccggttacta	tgtctctgtc	480
tgctaccatg	aggatgctgt	ccatatgggt	tgggttggtat	ggatgaatta	tattattcat	540
gcattcatgt	atggatacta	tcttctgaaa	tctctgaaag	ttccaattcc	accatcagtt	600
gctcaagcaa	tcaccacatc	tcaaattggt	caattcgcag	ttgccatttt	cgcacaagtt	660
catgtttcct	ataaacacta	tgttgaggga	gttgaaggat	tagcctactc	gttcagagga	720
acagctatcg	gatttttcat	gcttactacc	tacttctatc	tatggattca	attctacaaa	780
gagcactatc	ttaagaatgg	aggcaaaaag	tacaattttg	caaaggatca	ggcaaaaact	840
caaacaaaga	aggctaacta	a				861

<210> 11  
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 <213> C. elegans

<400> 11  
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 gttgtcggtta tttttgggct caaggctgtc atgacaaacc gaaaaccatt tgatctcacg 180  
 ggaccactga atctctggaa tgcgggtctt gctattttct caactctcgg atcacttgcc 240  
 actacatttg gacttctcca cgagttcttc agccgtggat ttttcgaatc ttacattcac 300  
 atcggagact tttataatgg actttctgga atgttcacat ggcttttctg tctctcaaaa 360  
 gttgctgaat tcggagatac actttttatt attcttcgta aaaagccatt gatgttcctt 420  
 cattgggtatc atcatgtgct tacaatgaat tatgctttta tgtcatttga agctaatttg 480  
 ggatttaata cttggattac atggatgaat ttctcagttc actcaattat gtatggatat 540  
 tatatgcttc gttcttttgg tgtcaagggt ccagcatgga ttgccaagaa tattacaaca 600  
 atgcaaattc ttcaattcgt tattactcat ttcatctctt tccacgttgg atatttgga 660  
 gttactggac aatctgttga ctcaactcca ggatattatt ggttctgcct tctcatggaa 720  
 atctcttatg tcgttctgtt cggaaacttc tactatcaat catacatcaa gggaggtggc 780  
 aagaagtta atgcagagaa gaagactgaa aagaaaattg aataa 825

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 <211> 846  
 <212> DNA  
 <213> C. elegans

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 gaattgtgga gtcttttaac gaatcaggat gaagttttcc cgcattattag agcacggcga 180  
 ttcatccaag aacatttttg tctattcgtc cagatggcaa ttgcatatgt cattttggtg 240  
 ttctcaatca aaaggttcat gagggatcgt gaaccatttc aactcaccac agctcttcgt 300  
 ctctggaact tcttctctc cgtcttctca atttatgggt cctggacaat gtttccattt 360  
 atggttcaac aaataagact ttatggtctc tacggatgtg gatgcgaagc actttcaaac 420  
 cttccgagtc aagcagaata ttggcttttc ctgacgatct tgtccaaagc tgtggagttt 480  
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 gtcggagtta tcgtcaacct gttcgtgcat gccttcatgt acccatacta tttcaccoga 660  
 tcaatgaaca tcaaagttcc tgcgaaaatt tcaatggctg ttacagttct tcaattgact 720  
 caattcatgt gctttatcta tggatgtact ctcatgtact actcgttggc cactaatcag 780  
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<210> 13  
 <211> 866  
 <212> DNA  
 <213> C. elegans

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gctgatcact ttgatgttac tattcaggct tcaatcctgt acatgggtcgt tgtgttcgga 180
acaaaatggg tcatgcgtaa tcgtcaacca ttccaattga ctattccact caacatctgg 240
aatttcattc tcgccgcatt ttccatcgca ggagctgtca aaatgacccc agagttcttt 300
ggaaccattg ccaacaaagg aattgtcgat cctactgcaa agtggttgat ttcacgaaag 360
gagagaatgg atactgggtg tggctcttca tggcttccaa acttttcgaa cttgttgaca 420
ccatcttctt gggttctccgt aaacgtccac tcatgttcct tcaactggat caccatattc 480
tcaccatgat ctacgcctgg tactctcatc cattgacccc aggattcaac agatacggaa 540
tttatcttaa ctttgtcgtc cacgccttca tgtactctta ctacttcctt cgctcgatga 600
agatttcgct gccaggattc atcgcccaag ctatcacatc tcttcaaadc gttcaattca 660
tcattctctt cgcgcgttct gctcatcttg gttatctcat gcacttcacc aatgccaact 720
gtgatttcga gccatcagta ttcaagctcg cagttttcat ggacacaaca tacttggtc 780
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cagtgcacaa gaagaagaac aactaa 866

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<210> 14  
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 <212> DNA  
 <213> C. elegans

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ctgcttatat tattgcgaca aattttattac agagatatat ggagtcacgg aaacctaata 180
cttttactag catggaacgg ttttttggca gtgttcagta ttatgggtac atggagattt 240
ggaatcgaat tctacgatgc tgttttcaga agaggcttca tcgattcgat ctgcctgggt 300
gtaaatccac gttcacccgc cgcattcttg gcatgcatgt tcgctctatc gaaaatcgcc 360
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tatcatcacg ctgttgttct gatcctttct tggcatgctg caatcgaact cacagctcca 480
ggacgctggt ttatttttat gaactatttg gtgcattcaa taatgtatac atactacgca 540
ataacatcaa tcggctatcg tcttcccaaa atcgtttcaa tgactgttac attccttcaa 600
actcttcaaa tgctcattgg tgtcagcatt tcttgcattg tgctttattt gaagcttaat 660
ggagagatgt gccacaatc ctacgacaat ctggcggttg gcttcggaat ctacgcctca 720
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cccgatgtga agaaggatta a 801

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<210> 15  
 <211> 291  
 <212> PRT  
 <213> C. elegans

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<400> 15
Met Glu Leu Ala Glu Phe Trp Asn Asp Leu Asn Thr Phe Thr Ile Tyr
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Gly Pro Asn His Thr Asp Met Thr Thr Lys Tyr Lys Tyr Ser Tyr His
          20             25             30

Phe Pro Gly Glu Gln Val Ala Asp Pro Gln Tyr Trp Thr Ile Leu Phe
          35             40             45

Gln Lys Tyr Trp Tyr His Ser Ile Thr Ile Ser Val Leu Tyr Phe Ile
          50             55             60

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Leu Ile Lys Val Ile Gln Lys Phe Met Glu Asn Arg Lys Pro Phe Thr  
65 70 75 80

Leu Lys Tyr Pro Leu Ile Leu Trp Asn Gly Ala Leu Ala Ala Phe Ser  
85 90 95

Ile Ile Ala Thr Leu Arg Phe Ser Ile Asp Pro Leu Arg Ser Leu Tyr  
100 105 110

Ala Glu Gly Phe Tyr Lys Thr Leu Cys Tyr Ser Cys Asn Pro Thr Asp  
115 120 125

Val Ala Ala Phe Trp Ser Phe Ala Phe Ala Leu Ser Lys Ile Val Glu  
130 135 140

Leu Gly Asp Thr Met Phe Ile Ile Leu Arg Lys Arg Pro Leu Ile Phe  
145 150 155 160

Leu His Tyr Tyr His His Ala Ala Val Leu Ile Tyr Thr Val His Ser  
165 170 175

Gly Ala Glu His Thr Ala Ala Gly Arg Phe Tyr Ile Leu Met Asn Tyr  
180 185 190

Phe Ala His Ser Leu Met Tyr Thr Tyr Tyr Thr Val Ser Ala Met Gly  
195 200 205

Tyr Arg Leu Pro Lys Trp Val Ser Met Thr Val Thr Thr Val Gln Thr  
210 215 220

Thr Gln Met Leu Ala Gly Val Gly Ile Thr Trp Met Val Tyr Lys Val  
225 230 235 240

Lys Thr Glu Tyr Lys Leu Pro Cys Gln Gln Ser Val Ala Asn Leu Tyr  
245 250 255

Leu Ala Phe Val Ile Tyr Val Thr Phe Ala Ile Leu Phe Ile Gln Phe  
260 265 270

Phe Val Lys Ala Tyr Ile Ile Lys Ser Ser Lys Lys Ser Lys Ser Val  
275 280 285

Lys Asn Glu  
290

<210> 16  
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<212> PRT  
<213> C. elegans

<400> 16  
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 Trp Met Gln Asn His Trp Tyr Gln Ser Ile Thr Ala Ser Val Val Tyr  
 35 40 45  
 Val Ala Val Ile Phe Thr Gly Lys Lys Val Val Leu Ile Tyr Lys Lys  
 50 55 60  
 Ser Arg Val Ile Thr Phe Glu Ser Ser Leu Gln Asn Ala Ile Lys Asn  
 65 70 75 80  
 Arg Asn Arg Lys Ser Leu Asn Ser Ser Gln Met Phe Gln Ile Met Glu  
 85 90 95  
 Lys Tyr Lys Pro Phe Gln Leu Asp Thr Pro Leu Phe Val Trp Asn Ser  
 100 105 110  
 Phe Leu Ala Ile Phe Ser Ile Leu Gly Phe Leu Arg Met Thr Pro Glu  
 115 120 125  
 Phe Val Trp Ser Trp Ser Ala Glu Gly Asn Ser Phe Lys Tyr Ser Ile  
 130 135 140  
 Cys His Ser Ser Tyr Ala Gln Gly Val Thr Gly Phe Trp Thr Glu Gln  
 145 150 155 160  
 Phe Ala Met Ser Lys Leu Phe Glu Leu Ile Asp Thr Ile Phe Ile Val  
 165 170 175  
 Leu Arg Lys Arg Pro Leu Ile Phe Leu His Trp Tyr His His Val Thr  
 180 185 190  
 Val Met Ile Tyr Thr Trp His Ala Tyr Lys Asp His Thr Ala Ser Gly  
 195 200 205  
 Arg Trp Phe Ile Trp Met Asn Tyr Gly Val His Ala Leu Met Tyr Ser  
 210 215 220  
 Tyr Tyr Ala Leu Arg Ser Leu Lys Phe Arg Leu Pro Lys Gln Met Ala  
 225 230 235 240  
 Met Val Val Thr Thr Leu Gln Leu Ala Gln Met Val Met Gly Val Ile  
 245 250 255  
 Ile Gly Val Thr Val Tyr Arg Ile Lys Ser Ser Gly Glu Tyr Cys Gln  
 260 265 270  
 Gln Thr Trp Asp Asn Leu Gly Leu Cys Phe Gly Val Tyr Phe Thr Tyr  
 275 280 285  
 Phe Leu Leu Phe Ala Asn Phe Phe Tyr His Ala Tyr Val Lys Lys Asn  
 290 295 300

Asn Arg Thr Val Asn Tyr Glu Asn Asn Ser Lys Asn Phe Pro Asp Leu  
 305 310 315 320  
 Val Leu Ile Tyr Leu Arg Lys Lys Val Ser Arg Lys Ser Lys Asn Arg  
 325 330 335  
 Gln Cys Ser Glu Asn Asn Tyr Lys Ile Gln Phe Ser Ser Asn Phe Val  
 340 345 350  
 Asn Val Asp Gly Lys Lys His Lys Lys Thr Tyr Glu Leu Ile Leu Pro  
 355 360 365  
 Arg Arg Lys Met Thr Thr Ile Leu Thr Phe Leu Phe Gly Lys Asn Arg  
 370 375 380  
 Ile Phe Ser Lys Tyr Gln Lys Asn Arg Lys Asn Ile Ser Ile Pro Val  
 385 390 395 400  
 Asp Phe Glu Ile Leu Glu Pro Lys Glu Asp Ile Asn Ala Asn Ile Ala  
 405 410 415  
 Glu Pro Ser Ile Thr Thr Arg Ser Ala Ala Ala Arg Arg Lys Val Gln  
 420 425 430  
 Lys Ala Asp  
 435  
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 <213> C. elegans  
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 35 40 45  
 Phe Gly Gln Lys Leu Met Ala His Arg Lys Pro Phe Asp Leu Gln Asn  
 50 55 60  
 Thr Leu Ala Leu Trp Asn Phe Gly Phe Ser Leu Phe Ser Gly Ile Ala  
 65 70 75 80  
 Ala Tyr Lys Leu Ile Pro Glu Leu Phe Gly Val Phe Met Lys Asp Gly  
 85 90 95  
 Phe Val Ala Ser Tyr Cys Gln Asn Glu Asn Tyr Tyr Thr Asp Ala Ser  
 100 105 110



Thr Gly Phe Trp Gly Trp Ala Phe Val Met Ser Lys Ala Pro Glu Leu  
115 120 125

Gly Asp Thr Met Phe Leu Val Leu Arg Lys Lys Pro Val Ile Phe Met  
130 135 140

His Trp Tyr His His Ala Leu Thr Phe Val Tyr Ala Val Val Thr Tyr  
145 150 155 160

Ser Glu His Gln Ala Trp Ala Arg Trp Ser Leu Ala Leu Asn Leu Ala  
165 170 175

Val His Thr Val Met Tyr Phe Tyr Phe Ala Val Arg Ala Leu Asn Ile  
180 185 190

Gln Thr Pro Arg Pro Val Ala Lys Phe Ile Thr Thr Ile Gln Ile Val  
195 200 205

Gln Phe Val Ile Ser Cys Tyr Ile Phe Gly His Leu Val Phe Ile Lys  
210 215 220

Ser Ala Asp Ser Val Pro Gly Cys Ala Val Ser Trp Asn Val Leu Ser  
225 230 235 240

Ile Gly Gly Leu Met Tyr Ile Ser Tyr Leu Phe Leu Phe Ala Lys Phe  
245 250 255

Phe Tyr Lys Ala Tyr Ile Gln Lys Arg Ser Pro Thr Lys Thr Ser Lys  
260 265 270

Gln Glu

<210> 18  
<211> 286  
<212> PRT  
<213> C. elegans

<400> 18  
Met Ser Ser Asp Asp Arg Gly Thr Arg Thr Phe Lys Met Met Asp Gln  
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20 25 30

Gly Leu Glu Gly Phe Ser Ala Lys Leu Ala Val Gly Tyr Ile Ala Thr  
35 40 45

Ile Phe Gly Leu Lys Tyr Tyr Met Lys Asp Arg Lys Ala Phe Asp Leu  
50 55 60

Ser Thr Pro Leu Asn Ile Trp Asn Gly Ile Leu Ser Thr Phe Ser Leu

65		70		75		80
Leu Gly Phe Leu Phe Thr Phe Pro Thr Leu Leu Ser Val Ile Arg Lys						
		85		90		95
Asp Gly Phe Ser His Thr Tyr Ser His Val Ser Glu Leu Tyr Thr Asp						
	100		105		110	
Ser Thr Ser Gly Tyr Trp Ile Phe Leu Trp Val Ile Ser Lys Ile Pro						
	115		120		125	
Glu Leu Leu Asp Thr Val Phe Ile Val Leu Arg Lys Arg Pro Leu Ile						
	130		135		140	
Phe Met His Trp Tyr His His Ala Leu Thr Gly Tyr Tyr Ala Leu Val						
	145		150		155	160
Cys Tyr His Glu Asp Ala Val His Met Val Trp Val Val Trp Met Asn						
		165		170		175
Tyr Ile Ile His Ala Phe Met Tyr Gly Tyr Tyr Leu Leu Lys Ser Leu						
		180		185		190
Lys Val Pro Ile Pro Pro Ser Val Ala Gln Ala Ile Thr Thr Ser Gln						
	195		200		205	
Met Val Gln Phe Ala Val Ala Ile Phe Ala Gln Val His Val Ser Tyr						
	210		215		220	
Lys His Tyr Val Glu Gly Val Glu Gly Leu Ala Tyr Ser Phe Arg Gly						
	225		230		235	240
Thr Ala Ile Gly Phe Phe Met Leu Thr Thr Tyr Phe Tyr Leu Trp Ile						
		245		250		255
Gln Phe Tyr Lys Glu His Tyr Leu Lys Asn Gly Gly Lys Lys Tyr Asn						
		260		265		270
Leu Ala Lys Asp Gln Ala Lys Thr Gln Thr Lys Lys Ala Asn						
	275		280		285	

<210> 19  
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 <212> PRT  
 <213> C. elegans

<400> 19  
 Met Pro Gln Gly Glu Val Ser Phe Phe Glu Val Leu Thr Thr Ala Pro  
 1 5 10 15  
 Phe Ser His Glu Leu Ser Lys Lys His Ile Ala Gln Thr Gln Tyr Ala  
 20 25 30

Ala Phe Trp Ile Ser Met Ala Tyr Val Val Val Ile Phe Gly Leu Lys  
           35                          40                          45  
 Ala Val Met Thr Asn Arg Lys Pro Phe Asp Leu Thr Gly Pro Leu Asn  
           50                          55                          60  
 Leu Trp Asn Ala Gly Leu Ala Ile Phe Ser Thr Leu Gly Ser Leu Ala  
       65                          70                          75                          80  
 Thr Thr Phe Gly Leu Leu His Glu Phe Phe Ser Arg Gly Phe Phe Glu  
                           85                          90                          95  
 Ser Tyr Ile His Ile Gly Asp Phe Tyr Asn Gly Leu Ser Gly Met Phe  
                           100                          105                          110  
 Thr Trp Leu Phe Val Leu Ser Lys Val Ala Glu Phe Gly Asp Thr Leu  
           115                          120                          125  
 Phe Ile Ile Leu Arg Lys Lys Pro Leu Met Phe Leu His Trp Tyr His  
           130                          135                          140  
 His Val Leu Thr Met Asn Tyr Ala Phe Met Ser Phe Glu Ala Asn Leu  
       145                          150                          155                          160  
 Gly Phe Asn Thr Trp Ile Thr Trp Met Asn Phe Ser Val His Ser Ile  
                           165                          170                          175  
 Met Tyr Gly Tyr Tyr Met Leu Arg Ser Phe Gly Val Lys Val Pro Ala  
           180                          185                          190  
 Trp Ile Ala Lys Asn Ile Thr Thr Met Gln Ile Leu Gln Phe Val Ile  
           195                          200                          205  
 Thr His Phe Ile Leu Phe His Val Gly Tyr Leu Ala Val Thr Gly Gln  
           210                          215                          220  
 Ser Val Asp Ser Thr Pro Gly Tyr Tyr Trp Phe Cys Leu Leu Met Glu  
       225                          230                          235                          240  
 Ile Ser Tyr Val Val Leu Phe Gly Asn Phe Tyr Tyr Gln Ser Tyr Ile  
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[illegible]

12

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 Asp Ala Glu Gly Arg Lys Phe Phe Ala Asp His Phe Asp Val Thr Ile  
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 Gln Ala Ser Ile Leu Tyr Met Val Val Val Phe Gly Thr Lys Trp Phe  
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 Met Arg Asn Arg Gln Pro Phe Gln Leu Thr Ile Pro Leu Asn Ile Trp  
 65 70 75 80  
 Asn Phe Ile Leu Ala Ala Phe Ser Ile Ala Gly Ala Val Lys Met Thr  
 85 90 95  
 Pro Glu Phe Phe Gly Thr Ile Ala Asn Lys Gly Ile Val Ala Ser Tyr  
 100 105 110  
 Cys Lys Val Phe Asp Phe Thr Lys Gly Glu Asn Gly Tyr Trp Val Trp  
 115 120 125  
 Leu Phe Met Ala Ser Lys Leu Phe Glu Leu Val Asp Thr Ile Phe Leu  
 130 135 140  
 Val Leu Arg Lys Arg Pro Leu Met Phe Leu His Trp Tyr His His Ile  
 145 150 155 160  
 Leu Thr Met Ile Tyr Ala Trp Tyr Ser His Pro Leu Thr Pro Gly Phe  
 165 170 175  
 Asn Arg Tyr Gly Ile Tyr Leu Asn Phe Val Val His Ala Phe Met Tyr  
 180 185 190  
 Ser Tyr Tyr Phe Leu Arg Ser Met Lys Ile Arg Val Pro Gly Phe Ile  
 195 200 205  
 Ala Gln Ala Ile Thr Ser Leu Gln Ile Val Gln Phe Ile Ile Ser Cys  
 210 215 220  
 Ala Val Leu Ala His Leu Gly Tyr Leu Met His Phe Thr Asn Ala Asn  
 225 230 235 240  
 Cys Asp Phe Glu Pro Ser Val Phe Lys Leu Ala Val Phe Met Asp Thr  
 245 250 255



Ser Ile Met Tyr Thr Tyr Tyr Ala Ile Thr Ser Ile Gly Tyr Arg Xaa  
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 Pro Lys Ile Val Ser Met Thr Val Thr Phe Leu Gln Thr Leu Gln Met  
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 Leu Ile Gly Val Ser Ile Ser Cys Ile Val Leu Tyr Leu Lys Leu Asn  
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 Gly Glu Met Cys Gln Gln Ser Tyr Asp Asn Leu Ala Leu Ser Phe Gly  
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 Leu Val Lys Lys Asp Lys Lys Pro Asp Val Lys Lys Asp  
 260 265